

# SEQUENCE LISTING

<110> Gentide Biopharmaceuticals, Inc.  
Russell, Stuart

<120> METHODS TO CONSTRUCT MULTIMERIC DNA AND POLYMERIC PROTEIN SEQUENCES AS  
DIRECT FUSIONS OR WITH LINKERS

<130> GNT-00101.P.1-US

<150> US 60/396,466

<151> 2002-07-16

<160> 86

<170> PatentIn version 3.0

<210> 1

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<212> DNA

<213> Homo sapiens

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Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg  
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Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu  
65 70 75 80

Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val  
85 90 95

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100 105 110

Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu  
115 120 125

Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser  
130 135 140

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr  
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Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe  
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Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	50	55	60	
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Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	130	135	140	
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Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	165	170	175	
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Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
 35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
 50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
 65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
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165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly  
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Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe  
35 40 45

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr  
50 55 60

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu  
65 70 75 80

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe  
85 90 95

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser  
100 105 110

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
115 120 125

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys  
130 135 140

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu  
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Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys  
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 gatgacgcac tactcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag 540  
 gtcgagacat tctgcgcat cgtgcagtg cgctctgtgg agggatcatg tggcttcttc 600  
 ccaaccattc cttatccag gctttttgac aacgctatgc tccgcgcccc tegtctgcac 660  
 cagctggcct ttgacaccta ccaggagttt gaagaagcct atatcccaaa ggaacagaag 720  
 tattcattcc tgcagaaccc ccagacctcc ctctgtttct cagagtctat tccgacaccc 780  
 tccaacaggg aggaaacaca acagaaatcc aacctagagc tgctccgcat ctccctgctg 840  
 ctcattccagt cgtggctgga gcccgctgag ttcttcagga gtgtcttcgc caacagcctg 900  
 gtgtacggcg cctctgacag caacgtctat gacctcctaa aggacctaga ggaaggcatc 960  
 caaacgctga tggggaggct ggaagatggc agcccccgga ctgggcagat cttcaagcag 1020  
 acctacagca agttcgacac aaactcacac aacgatgacg cactactcaa gaactacggg 1080  
 ctgctctact gcttcaggaa ggacatggac aaggctcgaga cattcctgcg catcgtgcag 1140  
 tgccgctctg tggagggatc c 1161

<210> 27

<211> 382

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<400> 27

Ser Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn  
 1 5 10 15

Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr  
 20 25 30

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe  
 35 40 45

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr  
 50 55 60

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu  
 65 70 75 80

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe  
 85 90 95

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser  
 100 105 110

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
 115 120 125

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys  
 130 135 140

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu  
 145 150 155 160

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys  
 165 170 175

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser  
 180 185 190

Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala  
 195 200 205

Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln  
 210 215 220

Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu  
 225 230 235 240

Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro  
 245 250 255

Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg  
 260 265 270

Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu  
 275 280 285

Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn  
 290 295 300

Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met  
 305 310 315 320

Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln  
 325 330 335

Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu  
 340 345 350

Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val  
 355 360 365

Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly  
 370 375 380

<210> 28  
 <211> 1152  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic sequence

<220>  
 <221> misc\_feature  
 <222> (574)..(1146)  
 <223> sequence is repeated N-1 times, where N is a positive whole numbe

<400> 28  
 tgatcatgtg gcttcttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc 60  
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 atcccāaaagg aacagaagta ttcattctctg cagaaccccc agacctccct ctgtttctca 180  
 gagtctattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg 240  
 ctccgcatct cctgtctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt 300  
 gtcttcgcca acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag 360  
 gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact 420  
 gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca 480  
 ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 540  
 ttcttgcgca tcgtgcagtg ccgctctgtg gagggatcat gtggcttctt cccaaccatt 600  
 cccttatcca ggctttttga caacgctatg ctccgcgccc atcgtctgca ccagctggcc 660  
 tttgacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa gtattcattc 720  
 ctgcagaacc cccagacctc cctctgtttc tcagagtcta ttccgacacc ctccaacagg 780  
 gaggaacac aacagaaatc caacctagag ctgctccgca tctcctgct gctcatccag 840  
 tcgtggctgg agcccgctgca gttcctcagg agtgtcttcg ccaacagcct ggtgtacggc 900  
 gcctctgaca gcaacgtcta tgacctcta aaggacctag aggaaggcat ccaaacgctg 960  
 atggggaggc tggaagatgg cagcccccg actgggcaga tcttcaagca gacctacagc 1020  
 aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg gctgctctac 1080



tgcttcagga aggacatgga caaggtcgag acattcctgc gcatcgtgca gtgccgctct 1140

gtggagggat cc 1152

<210> 29

<211> 382

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC\_FEATURE

<222> (191)..(381)

<223> sequence is repeated N-1 times, where N is a positive whole numbe

<400> 29

Ser Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn  
1 5 10 15

Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr  
20 25 30

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe  
35 40 45

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr  
50 55 60

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu  
65 70 75 80

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe  
85 90 95

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser  
100 105 110

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
115 120 125

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys  
130 135 140

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu  
145 150 155 160

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys  
165 170 175

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser



aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag	360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc	420
ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag	480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc	540
atcgtgcagt gccgctctgt ggagggatcc gaattccatt gatcatgtgg cttctagtag	600
gtcgac	606

<210> 31  
 <211> 1737  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> synthetic sequence  
  
 <220>  
 <221> misc\_feature  
 <222> (1138)..(1710)  
 <223> sequence is repeated N-1 times, where N is a positive whole number

<400> 31	
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cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag	120
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt	180
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac	240
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc	300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag	360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc	420
ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag	480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc	540
atcgtgcagt gccgctctgt ggagggatca tgtggcttct tcccaaccat tcccttatcc	600
aggctttttg acaacgctat gctccgcgcc catcgtctgc accagctggc ctttgacacc	660
taccaggagt ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac	720
ccccagacct ccctctgttt ctgagagtct attccgacac cctccaacag ggaggaaaca	780
caacagaaat ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg	840

gagcccggtgc agttcctcag gagtgtcttc gccaacagcc tgggtgtacgg cgcctctgac 900  
 agcaacgtct atgacctcct aaaggacctt gaggaaggca tccaaacgct gatggggagg 960  
 ctggaagatg gcagcccccg gactgggcag atcttcaagc agacctacag caagtctgac 1020  
 acaaactcac acaacgatga cgcactactc aagaactacg ggctgctcta ctgcttcagg 1080  
 aaggacatgg acaaggtcga gacattcctg cgcacgtgc agtgccgctc tgtggaggga 1140  
 tcatgtggct tcttcccaac cattccctta tccaggcttt ttgacaacgc tatgctccgc 1200  
 gcccatcgtc tgcaccagct ggcctttgac acctaccagg agtttgaaga agcctatata 1260  
 ccaaaggaac agaagtattc attcctgcag aacccccaga cctccctctg tttctcagag 1320  
 tctattccga caccctccaa cagggaggaa acacaacaga aatccaacct agagctgctc 1380  
 cgcactctcc tgcgtctcat ccagtcgtgg ctggagcccg tgcagttcct caggagtgtc 1440  
 ttgcgaaca gcctgggtgta cggcgctctt gacagcaacg tctatgacct cctaaaggac 1500  
 ctagaggaag gcatccaaac gctgatgggg aggctggaag atggcagccc ccggactggg 1560  
 cagatcttca agcagacctt cagcaagttc gacacaaact cacacaacga tgacgcacta 1620  
 ctcaagaact acggggtgct ctactgcttc aggaaggaca tggacaaggc cgagacattc 1680  
 ctgcgcacgc tgcagtgccg ctctgtggag ggatcatgtg gcttctagta ggctcgac 1737

<210> 32  
 <211> 574  
 <212> PRT  
 <213> Artificial

<220>  
 <223> synthetic sequence

<220>  
 <221> MISC\_FEATURE  
 <222> (379)..(569)  
 <223> sequence is repeated N-1 times, where N is a positive whole number

<220>  
 <221> mat\_peptide  
 <222> (1)..()

<400> 32

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
 1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
 20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
 35 40 45  
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
 50 55 60  
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
 65 70 75 80  
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
 85 90 95  
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
 100 105 110  
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
 115 120 125  
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
 130 135 140  
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
 145 150 155 160  
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
 165 170 175  
 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
 180 185 190  
 Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg  
 195 200 205  
 Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu  
 210 215 220  
 Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro  
 225 230 235 240  
 Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg  
 245 250 255  
 Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu  
 260 265 270  
 Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val  
 275 280 285  
 Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp  
 290 295 300  
 Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu  
 305 310 315 320  
 Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser  
 325 330 335

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr  
 340 345 350  
 Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe  
 355 360 365  
 Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Phe  
 370 375 380  
 Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala  
 385 390 395 400  
 His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu  
 405 410 415  
 Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln  
 420 425 430  
 Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu  
 435 440 445  
 Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu  
 450 455 460  
 Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe  
 465 470 475 480  
 Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu  
 485 490 495  
 Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu  
 500 505 510  
 Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys  
 515 520 525  
 Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly  
 530 535 540  
 Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu  
 545 550 555 560  
 Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
 565 570

<210> 33

<211> 55

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 33

taccatgatga catgatcatg tggcttcggg ttcccaacca ttcccttata caggc

<210> 34  
<211> 591  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 34  
catatgacat gatcatgtgg cttcggtttc ccaaccattc ccttatccag gctttttgac 60  
aacgctatgc tccgcgcccc tcgtctgcac cagctggcct ttgacaccta ccaggagttt 120  
gaagaagcct atatcccaaa ggaacagaag tattcattcc tgcagaaccc ccagacctcc 180  
ctctgtttct cagagtctat tccgacaccc tccaacaggg aggaaacaca acagaaatcc 240  
aacctagagc tgctccgcat ctccctgctg ctcatccagt cgtggctgga gcccgctgcag 300  
ttcctcagga gtgtcttcgc caacagcctg gtgtacggcg cctctgacag caacgtctat 360  
gacctcctaa aggacctaga ggaaggcatc caaacgctga tggggaggct ggaagatggc 420  
agcccccgga ctgggcagat cttcaagcag acctacagca agttcgacac aaactcacac 480  
aacgatgacg cactactcaa gaactacggg ctgctctact gcttcaggaa ggacatggac 540  
aaggtcgaga cattcctgcg catcgtgcag tgccgctctg tggagggatc c 591

<210> 35  
<211> 192  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 35

Ser Cys Gly Phe Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp  
1 5 10 15

Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr  
20 25 30

Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser  
35 40 45

Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro  
50 55 60

Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu  
65 70 75 80

Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln

Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp  
100 105 110

Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr  
115 120 125

Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe  
130 135 140

Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala  
145 150 155 160

Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp  
165 170 175

Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly  
180 185 190

<210> 36

<211> 1158

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc\_feature

<222> (577)..(1152)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 36

tgatcatgtg gcttcggttt cccaaccatt cccttatcca ggctttttga caacgctatg 60

ctccgcgccc atcgtctgca ccagctggcc tttgacacct accaggagtt tgaagaagcc 120

tatatcccaa aggaacagaa gtattcattc ctgcagaacc ccagacctc cctctgtttc 180

tcagagtcta ttccgacacc ctccaacagg gaggaacac aacagaaatc caacctagag 240

ctgctccgca tctccctgct gctcatccag tcgtggctgg agcccgtgca gttcctcagg 300

agtgtcttcg ccaacagcct ggtgtacggc gcctctgaca gcaacgtcta tgacctccta 360

aaggacctag aggaaggcat ccaaacgctg atggggaggc tggaagatgg cagcccccg 420

actgggcaga tcttcaagca gacctacagc aagttcgaca caaactcaca caacgatgac 480

gcactactca agaactacgg gctgctctac tgcttcagga aggacatgga caaggctcag 540

acattcctgc gcacgtgca gtgccgctct gtggagggat catgtggctt cggtttccca 600

accattccct tatccaggct ttttgacaac gctatgctcc gcgcccatcg tctgcaccag 660



ctggcctttg acacctacca ggagtttgaa gaagcctata tcccaaagga acagaagtat 720  
 tcattcctgc agaaccacca gacctccctc tgtttctcag agtctattcc gacaccctcc 780  
 aacagggagg aaacacaaca gaaatccaac ctagagctgc tccgcatctc cctgctgctc 840  
 atccagtcgt ggctggagcc cgtgcagttc ctcaggagtg tcttcgcca cagcctgggtg 900  
 tacggcgcct ctgacagcaa cgtctatgac ctctaaagg acctagagga aggcattccaa 960  
 acgctgatgg ggaggctgga agatggcagc ccccgactg ggagatctt caagcagacc 1020  
 tacagcaagt tcgacacaaa ctacacaaac gatgacgcac tactcaagaa ctacgggctg 1080  
 ctctactgct tcaggaagga catggacaag gtcgagacat tctgcgcat cgtgcagtgc 1140  
 cgctctgtgg agggatcc 1158

<210> 37  
 <211> 384  
 <212> PRT  
 <213> Artificial

<220>  
 <223> synthetic sequence

<220>  
 <221> MISC\_FEATURE  
 <222> (192)..(383)  
 <223> sequence is repeated N-1 times, where N is a positive whole number

<400> 37

Ser	Cys	Gly	Phe	Gly	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp
1				5					10					15	
Asn	Ala	Met	Leu	Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr
			20					25					30		
Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser
	35						40				45				
Phe	Leu	Gln	Asn	Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro
	50					55				60					
Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu
65					70					75				80	
Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln
			85					90					95		
Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp
	100						105						110		

Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr  
115 120 125

Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe  
130 135 140

Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala  
145 150 155 160

Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp  
165 170 175

Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly  
180 185 190

Ser Cys Gly Phe Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp  
195 200 205

Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr  
210 215 220

Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser  
225 230 235 240

Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro  
245 250 255

Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu  
260 265 270

Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln  
275 280 285

Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp  
290 295 300

Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr  
305 310 315 320

Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe  
325 330 335

Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala  
340 345 350

Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp  
355 360 365

Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly  
370 375 380

<210> 38  
<211> 1743  
<212> DNA  
<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc\_feature

<222> (1141)..(1716)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 38

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gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt      180
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcatc      240
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc      300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag      360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc      420
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag      480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc      540
atcgtgcagt gccgctctgt ggagggatca tgtggcttcg gtttcccaac cattccctta      600
tccaggcttt ttgacaacgc tatgctccgc gcccatcgtc tgcaccagct ggcctttgac      660
acctaccagg agtttgaaga agcctatatc ccaaaggaa acagaatttc attcctgcag      720
aacccccaga cctcctctg tttctcagag tctattccga caccctccaa caggaggagaa      780
acacaacaga aatccaacct agagctgctc cgcctctccc tgctgctcat ccagtcgtgg      840
ctggagcccc tgcagttcct caggagtgtc ttgcgcaaca gcttggtgta cggcgctctc      900
gacagcaacg tctatgacct cctaaaggac ctagaggaag gcatccaaac gctgatgggg      960
aggctggaag atggcagccc ccggactggg cagatcttca agcagacctc cagcaagttc     1020
gacacaaact cacacaacga tgacgcacta ctcaagaact acgggctgct ctactgcttc     1080
aggaaggaca tggacaaggt cgagacattc ctgcgcctcg tgcagtgccg ctctgtggag     1140
ggatcatgtg gcttcggttt cccaaccatt cccttatcca ggctttttga caacgctatg     1200
ctccgcgccc atcgtctgca ccagctggcc ttgacacct accaggagtt tgaagaagcc     1260
tatatcccaa aggaacagaa gtattcattc ctgcagaacc ccagacctc cctctgtttc     1320
tcagagtcta ttccgacacc ctccaacagg gaggaacac aacagaaatc caacctagag     1380
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```

ctgctccgca tctccctgct gctcatccag tegtggctgg agcccggtgca gttcctcagg 1440
agtgtcttcg ccaacagcct ggtgtacggc gcctctgaca gcaacgtcta tgacctccta 1500
aaggacctag aggaaggcat ccaaacgctg atggggaggc tggaagatgg cagcccccg 1560
actgggcaga tcttcaagca gacctacagc aagttcgaca caaactcaca caacgatgac 1620
gcactactca agaactacgg gctgctctac tgcttcagga aggacatgga caaggctcag 1680
acattcctgc gcatcgtgca gtgccgctct gtggagggat catgtggctt ctagtaggtc 1740
gac 1743

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<210> 39
<211> 576
<212> PRT
<213> Artificial

<220>
<223> synthetic sequence

<220>
<221> MISC_FEATURE
<222> (380)..(571)
<223> sequence is repeated N-1 times, where N is a positive whole numbe

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<220>
<221> mat_peptide
<222> (1)..()

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<400> 39

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Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1      5      10      15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
      20      25      30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
      35      40      45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
      50      55      60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65      70      75      80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
      85      90      95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
      100      105      110

```

Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg		
	115						120					125					
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr		
	130					135					140						
Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn		
145					150				155						160		
Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr		
			165						170					175			
Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe		
		180						185					190				
Gly	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu		
	195						200					205					
Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe		
	210					215					220						
Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn		
225					230					235					240		
Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn		
			245						250					255			
Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser		
			260					265					270				
Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser		
	275						280					285					
Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr		
	290					295					300						
Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg		
305					310					315					320		
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr		
			325						330					335			
Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn		
		340						345					350				
Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr		
	355						360					365					
Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe		
	370					375					380						
Gly	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu		
385					390					395					400		
Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe		
				405					410					415			

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
 420 425 430

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
 435 440 445

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
 450 455 460

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
 465 470 475 480

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
 485 490 495

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
 500 505 510

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
 515 520 525

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
 530 535 540

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
 545 550 555 560

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
 565 570 575

<210> 40  
 <211> 39  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 40  
 cgcggatcct catgagaagc cacagctgcc ctccacaga

39

<210> 41  
 <211> 591  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 41  
 catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccat

60

cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag

120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt

180

ccgacaccct ccaacagggg ggaacacaaa cagaaatcca acctagagct gctccgcac 240  
 tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc 300  
 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360  
 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420  
 ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480  
 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540  
 atcgtgcagt gccgtctgt ggagggcagc tgtggcttct catgaggatc c 591

<210> 42  
 <211> 193  
 <212> PRT  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 42

Met	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu
1				5					10					15	
Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe
			20					25					30		
Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn
		35					40					45			
Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn
		50				55					60				
Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser
65					70					75					80
Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser
			85						90					95	
Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr
			100					105					110		
Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg
		115					120					125			
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr
		130				135						140			
Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn
145					150					155					160
Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr
			165						170					175	

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Ser

<210> 43  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 43  
catgccatgg ggtgggtggag gaagtttccc aaccattccc ttatccaggc 50

<210> 44  
<211> 606  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 44  
ccatgggggtg gtggaggaag ttccccaacc attcccttat ccaggctttt tgacaacgct 60  
atgctccgcg cccatcgtct gcaaccagctg gcctttgaca cctaccagga gtttgaagaa 120  
gcctatatcc caaaggaaca gaagtattca ttcttgaga accccagac ctccctctgt 180  
ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta 240  
gagctgctcc gcctctccct gctgctcatc cagtcgtggc tggagcccgt gcagttcctc 300  
aggagtgtct tcgccaacag cctgggtgtac ggccgctctg acagcaacgt ctatgacctc 360  
ctaaaggacc tagaggaagg catccaaacg ctgatgggga ggctggaaga tggcagcccc 420  
cggactgggc agatcttcaa gcagacctac agcaagttcg acacaaactc acacaacgat 480  
gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc 540  
gagacattcc tgcgcacgtg gcagtgccgc tctgtggagg gcagctgtgg cttctcatga 600  
ggatcc 606

<210> 45  
<211> 198  
<212> PRT  
<213> Artificial

<220>



<223> synthetic sequence

<400> 45

Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe  
1 5 10 15

Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp  
20 25 30

Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr  
35 40 45

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile  
50 55 60

Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu  
65 70 75 80

Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val  
85 90 95

Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser  
100 105 110

Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln  
115 120 125

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile  
130 135 140

Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp  
145 150 155 160

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met  
165 170 175

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu  
180 185 190

Gly Ser Cys Gly Phe Ser  
195

<210> 46

<211> 603

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 46

ccatgggggtg gtggaggaag tttcccaacc attcccttat ccaggctttt tgacaacgct 60

atgctccgcg cccatcgctc gcaccagctg gcctttgaca cctaccagga gtttgaagaa 120

gcctatatcc caaaggaaca gaagtattca ttctgcaga acccccagac ctccctctgt 180

ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta 240  
 gagctgctcc gcattctcct gctgctcacc cagtcgtggc tggagcccgt gcagttcctc 300  
 aggagtgtct tcgccaacag cctgggtgtac ggcgcctctg acagcaacgt ctatgacctc 360  
 ctaaaggacc tagaggaagg catccaaacg ctgatgggga ggctggaaga tggcagcccc 420  
 cggactgggc agatcttcaa gcagacctac agcaagttcg acacaaactc acacaacgat 480  
 gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc 540  
 gagacattcc tgcgcatcgt gcagtgccgc tctgtggagg gcagctgtgg cttctagggg 600  
 tcc 603

<210> 47  
 <211> 197  
 <212> PRT  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 47

Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe  
 1 5 10 15  
 Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp  
 20 25 30  
 Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr  
 35 40 45  
 Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile  
 50 55 60  
 Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu  
 65 70 75 80  
 Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val  
 85 90 95  
 Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser  
 100 105 110  
 Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln  
 115 120 125  
 Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile  
 130 135 140  
 Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp  
 145 150 155 160

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met  
 165 170 175

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu  
 180 185 190

Gly Ser Cys Gly Phe  
 195

<210> 48

<211> 1200

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc feature

<222> (595)..(1188)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 48

ccatgggggtg gtggaggaag tttcccaacc attcccttat ccaggctttt tgacaacgct 60  
 atgctccgcg cccatcgtct gcaccagctg gcctttgaca cctaccagga gtttgaagaa 120  
 gcctatatcc caaaggaaca gaagtattca ttcctgcaga acccccagac ctccctctgt 180  
 ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta 240  
 gagctgctcc gcattctcct gctgctcatc cagtcgtggc tggagcccgt gcagttcctc 300  
 aggagtgtct tcgccaacag cctggtgtac ggcgcctctg acagcaacgt ctatgacctc 360  
 ctaaaggacc tagaggaagg catccaaacg ctgatgggga ggctggaaga tggcagcccc 420  
 cggactgggc agatcttcaa gcagacctac agcaagttcg acacaaactc acacaacgat 480  
 gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc 540  
 gagacattcc tgcgcatcgt gcagtgccgc tctgtggagg gcagctgtgg cttctcatgg 600  
 ggtggtggag gaagtttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc 660  
 cgcgcccatc gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat 720  
 atcccaaagg aacagaagta ttcattcctg cagaaccccc agacctcct ctgtttctca 780  
 gagtctattc cgacacctc caacaggag gaaacacaac agaaatccaa cctagagctg 840  
 ctccgcatct cctgctgct catccagtcg tggtggagc ccgtgcagtt cctcaggagt 900  
 gtcttcgcca acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag 960

gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact 1020  
 gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca 1080  
 ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 1140  
 ttcttgcgca tcgtgcagtg ccgctctgtg gagggcagct gtggcttctc atgaggatcc 1200

<210> 49

<211> 396

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC FEATURE

<222> (198)..(395)

<223> sequence is repeated N-1 times, where N is a positive whole numbe

<400> 49

Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe  
 1 5 10 15

Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp  
 20 25 30

Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr  
 35 40 45

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile  
 50 55 60

Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu  
 65 70 75 80

Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val  
 85 90 95

Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser  
 100 105 110

Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln  
 115 120 125

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile  
 130 135 140

Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp  
 145 150 155 160

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met  
 165 170 175

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu  
 180 185 190

Gly Ser Cys Gly Phe Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile  
 195 200 205

Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu  
 210 215 220

His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile  
 225 230 235 240

Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu  
 245 250 255

Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln  
 260 265 270

Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln  
 275 280 285

Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser  
 290 295 300

Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp  
 305 310 315 320

Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser  
 325 330 335

Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr  
 340 345 350

Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr  
 355 360 365

Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val  
 370 375 380

Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Ser  
 385 390 395

<210> 50

<211> 1185

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 50

catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccat 60

cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag 120

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gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180
ccgacaccct ccaacagggg ggaaacacaa cagaaatcca acctagagct gctccgcatc 240
tccttgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc 300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gcccccgac tgggcagatc 420
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540
atcgtgcagt gccgctctgt ggagggcagc tgtgggttct catgggggtg tggaggaagt 600
ttcccaacca ttcccttatt caggcttttt gacaacgcta tgctccgcgc ccatcgtctg 660
caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag 720
aagtattcat tcctgcagaa cccccagacc tcctctgtt tctcagagtc tattccgaca 780
ccctccaaca gggaggaaac acaacagaaa tccaacctag agctgctccg catctccctg 840
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atccaaacgc tgatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag 1020
cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac 1080
gggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcacgtg 1140
cagtgccgct ctgtggaggg cagctgtggc ttctcatgag gatcc 1185

```

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<210> 51
<211> 391
<212> PRT
<213> Artificial

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<220>
<223> synthetic sequence

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<220>
<221> mat_peptide
<222> (1)..()

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<400> 51

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Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1           5           10          15
Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20          25          30

```

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
 35 40 45  
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
 50 55 60  
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
 65 70 75 80  
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
 85 90 95  
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
 100 105 110  
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
 115 120 125  
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
 130 135 140  
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
 145 150 155 160  
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
 165 170 175  
 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
 180 185 190  
 Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu  
 195 200 205  
 Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe  
 210 215 220  
 Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys  
 225 230 235 240  
 Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser  
 245 250 255  
 Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu  
 260 265 270  
 Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro  
 275 280 285  
 Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala  
 290 295 300  
 Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile  
 305 310 315 320  
 Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln  
 325 330 335

Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp  
340 345 350

Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp  
355 360 365

Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val  
370 375 380

Glu Gly Ser Cys Gly Phe Ser  
385 390

<210> 52

<211> 1779

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc\_feature

<222> (1174)..(1767)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 52

catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccat 60

cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag 120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180

ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac 240

tccctgctgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc 300

aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360

gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420

ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480

aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540

atcgtgcagt gccgctctgt ggagggcagc tgtggcttct catgggggtg tggaggaagt 600

ttcccaacca ttcccttatc caggcttttt gacaacgcta tgctccgcgc ccatcgtctg 660

caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag 720

aagtattcat tctgcagaa ccccagacc tccctctgtt tctcagagtc tattccgaca 780

ccctccaaca gggaggaaac acaacagaaa tccaacctag agctgctccg catctccctg 840



ctgctcatcc agtcgtggct ggagcccgct cagttcctca ggagtgtctt cgccaacagc 900  
 ctgggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggc 960  
 atccaaacgc tgatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag 1020  
 cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac 1080  
 gggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcacgtg 1140  
 cagtgccgct ctgtggaggg cagctgtggc ttctcatggg gtgggtggagg aagtttccca 1200  
 accattccct tatccaggct ttttgacaac gctatgctcc gcgcccacg tctgcaccag 1260  
 ctggcctttg acacctacca ggagtttgaa gaagcctata tcccaaagga acagaagtat 1320  
 tcattcctgc agaaccacca gacctccctc tgtttctcag agtctattcc gacacctcc 1380  
 aacagggagg aaacacaaca gaaatccaac ctgagagtgc tccgcatctc cctgctgctc 1440  
 atccagtcgt ggctggagcc cgtgcagttc ctgaggagtg tcttcgcca cagcctgggtg 1500  
 tacggcgct ctgacagcaa cgtctatgac ctctaaagg acctagagga aggcattcaa 1560  
 acgctgatgg ggaggctgga agatggcagc ccccgactg ggcagatctt caagcagacc 1620  
 tacagcaagt tcgacacaaa ctacacaaac gatgacgcac tactcaagaa ctacgggctg 1680  
 ctctactgct tcaggaagga catggacaag gtcgagacat tcctgcgcat cgtgcagtgc 1740  
 cgctctgtgg agggcagctg tggcttctca tgaggatcc 1779

<210> 53

<211> 589

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC\_FEATURE

<222> (391)..(588)

<223> sequence is repeated N-1 times, where N is a positive whole numbe

<220>

<221> mat\_peptide

<222> (1)..()

<400> 53

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
 1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
 20 25 30  
 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
 35 40 45  
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
 50 55 60  
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
 65 70 75 80  
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
 85 90 95  
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
 100 105 110  
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
 115 120 125  
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
 130 135 140  
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Ala Leu Leu Lys Asn  
 145 150 155 160  
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
 165 170 175  
 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
 180 185 190  
 Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu  
 195 200 205  
 Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe  
 210 215 220  
 Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys  
 225 230 235 240  
 Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser  
 245 250 255  
 Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu  
 260 265 270  
 Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro  
 275 280 285  
 Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala  
 290 295 300  
 Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile  
 305 310 315 320

Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln  
325 330 335

Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp  
340 345 350

Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp  
355 360 365

Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val  
370 375 380

Glu Gly Ser Cys Gly Phe Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr  
385 390 395 400

Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg  
405 410 415

Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr  
420 425 430

Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser  
435 440 445

Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr  
450 455 460

Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile  
465 470 475 480

Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn  
485 490 495

Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys  
500 505 510

Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly  
515 520 525

Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp  
530 535 540

Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu  
545 550 555 560

Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile  
565 570 575

Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Ser  
580 585

<210> 54

<211> 2370

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc\_feature

<222> (1174)..(1767)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 54

catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac	60
cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tateccaaag	120
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt	180
ccgacaccct ccaacagggg ggaacacaaa cagaaatcca acctagagct gctccgcac	240
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc	300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag	360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc	420
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag	480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc	540
atcgtgcagt gccgctctgt ggagggcagc tgtggcttct catgggggtg tggaggaagt	600
ttcccaacca ttcccttacc caggcttttt gacaacgcta tgctccgcgc ccacgtctctg	660
caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag	720
aagtattcat tctgcagaa cccccagacc tccctctgtt tctcagagtc tattccgaca	780
ccctccaaca gggaggaaac acaacagaaa tccaacctag agctgctccg catctccctg	840
ctgctcatcc agtcgtggct ggagcccgtg cagttcctca ggagtgtctt cgccaacagc	900
ctggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggc	960
atccaaacgc tgatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag	1020
cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac	1080
gggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcacgtg	1140
cagtgccgct ctgtggaggg cagctgtggc ttctcatggg gtggtggagg aagtttccca	1200
accattccct tatccaggct ttttgacaac gctatgctcc gcgcccatcg tctgcaccag	1260
ctggcctttg acacctacca ggagtttgaa gaagcctata tcccaaagga acagaagtat	1320
tcattcctgc agaaccacca gacctccctc tgtttctcag agtctattcc gacacctcc	1380
aacagggagg aaacacaaca gaaatccaac ctagagctgc tccgcatctc cctgctgctc	1440

atccagtcgt ggctggagcc cgtgcagttc ctcaggagtg tcttcgccaa cagcctggtg 1500  
 tacggcgcct ctgacagcaa cgtctatgac ctccataagg acctagagga aggcattccaa 1560  
 acgctgatgg ggaggctgga agatggcagc ccccgactg ggcagatctt caagcagacc 1620  
 tacagcaagt tcgacacaaa ctcacacaac gatgacgcac tactcaagaa ctacgggctg 1680  
 ctctactgct tcaggaagga catggacaag gtcgagacat tcctgcgcat cgtgcagtgc 1740  
 cgctctgtgg agggcagctg tggcttctca tggggtggtg gaggaagttt cccaaccatt 1800  
 cccttatcca ggctttttga caacgctatg ctccgcgccc atcgtctgca ccagctggcc 1860  
 tttgacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa gtattcattc 1920  
 ctgcagaacc cccagacctc cctctgtttc tcagagtcta ttccgacacc ctccaacagg 1980  
 gaggaaacac aacagaaatc caacctagag ctgctccgca tctccctgct gctcatccag 2040  
 tcgtggctgg agcccgtgca gttcctcagg agtgtcttcg ccaacagcct ggtgtacggc 2100  
 gcctctgaca gcaacgtcta tgacctcta aaggacctag aggaaggcat ccaaacgctg 2160  
 atggggaggc tggaagatgg cagcccccg actgggcaga ttttcaagca gacctacagc 2220  
 aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg gctgctctac 2280  
 tgcttcagga aggacatgga caaggtcgag acattcctgc gcacgtgca gtgccgctct 2340  
 gtggagggca gctgtggctt ctagggatcc 2370

<210> 55  
 <211> 786  
 <212> PRT  
 <213> Artificial

<220>  
 <223> synthetic sequence

<220>  
 <221> MISC\_FEATURE  
 <222> (391)..(588)

<220>  
 <221> mat\_peptide  
 <222> (1)..()

<400> 55

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
 1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
 20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
 35 40 45  
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
 50 55 60  
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
 65 70 75 80  
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
 85 90 95  
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
 100 105 110  
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
 115 120 125  
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
 130 135 140  
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
 145 150 155 160  
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
 165 170 175  
 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
 180 185 190  
 Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu  
 195 200 205  
 Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe  
 210 215 220  
 Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys  
 225 230 235 240  
 Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser  
 245 250 255  
 Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu  
 260 265 270  
 Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro  
 275 280 285  
 Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala  
 290 295 300  
 Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile  
 305 310 315 320  
 Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln  
 325 330 335

Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp
			340					345					350		
Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp
		355					360					365			
Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val
		370				375					380				
Glu	Gly	Ser	Cys	Gly	Phe	Ser	Trp	Gly	Gly	Gly	Gly	Ser	Phe	Pro	Thr
385					390					395					400
Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu	Arg	Ala	His	Arg
				405					410					415	
Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr
			420					425					430		
Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln	Thr	Ser
		435					440					445			
Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr
	450					455					460				
Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile
465					470					475					480
Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn
				485					490					495	
Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys
			500					505					510		
Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	Asp	Gly
		515					520					525			
Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp
						535					540				
Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu
545					550					555					560
Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	Arg	Ile
				565					570					575	
Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe	Ser	Trp	Gly	Gly
			580					585					590		
Gly	Gly	Ser	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala
		595					600					605			
Met	Leu	Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln
						615					620				
Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu
625					630					635					640

Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro  
645 650 655

Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg  
660 665 670

Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu  
675 680 685

Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn  
690 695 700

Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met  
705 710 715 720

Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln  
725 730 735

Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu  
740 745 750

Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val  
755 760 765

Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys  
770 775 780

Gly Phe  
785

<210> 56  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 56  
ttaccatgga ttgccggcgg cggcggatcc aat

33

<210> 57  
<211> 36  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 57  
ttaccatgga tttgatcagg cggcggcgga tccaat

36

<210> 58  
<211> 36



<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 58  
tgatcaggcg gcggcgatc aggcggcggc ggatcc

36

<210> 59  
<211> 10  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 59

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
1 5 10

<210> 60  
<211> 48  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 60  
gcggcgggcg gcggatcagg cggcggcgga tcaggcggcg gcggatcc

48

<210> 61  
<211> 14  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 61

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
1 5 10

<210> 62  
<211> 43  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 62

ggacatatgc tgtgatcatt cccaaccatt cccttatcca ggc

43

<210> 63

<211> 41

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 63

cgcgattcgc atccatggaa gccacagctg ccctccacag a

41

<210> 64

<211> 36

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 64

cgcgctcgacc tagaagccac agctgccctc cacaga

36

<210> 65

<211> 602

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 65

catatgctgt gatcattccc aaccattccc ttatccaggc tttttgacaa cgctatgctc 60

cgcgcccatc gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat 120

atcccaaagg aacagaagta ttcattctcg cagaaccccc agacctccct ctgtttctca 180

gagtctattc cgacacctc caacagggag gaaacacaac agaaatccaa cctagagctg 240

ctccgcatct ccttgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt 300

gtcttcgcca acagcctggg gtacggcgcc tctgacagca acgtctatga cctcctaaag 360

gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact 420

gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca 480

ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 540

ttcctgcgca tcgtgcagtg ccgctctgtg gagggcagct gtggcttcca tggatcgaat 600

tc

602

<210> 66  
<211> 192  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 66

Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

<210> 67  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 67

catatgctgt gatcattccc aaccattccc ttatccaggc tttttgacaa cgctatgctc 60  
cgcgcccatc gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat 120  
atcccaaagg aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca 180  
gagtctattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg 240  
ctccgcatct cctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt 300  
gtcttcgcca acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag 360  
gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact 420  
gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca 480  
ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 540  
ttcctgcgca tcgtgcagtg ccgctctgtg gagggcagct gtggcttcta ggtcgacgcg 600

<210> 68  
<211> 192  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 68

Ser	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu
1				5					10					15	
Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe
		20						25					30		
Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn
		35					40					45			
Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn
		50				55					60				
Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser
65				70						75				80	
Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser
			85						90					95	
Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr
		100						105					110		
Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg
		115				120						125			
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr
		130				135						140			

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
 145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
 165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
 180 185 190

<210> 69  
 <211> 639  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 69  
 catatgctgt gatcattccc aaccattccc ttatccaggc tttttgacaa cgctatgctc 60  
 cgcgcccatc gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat 120  
 atcccaaagg aacagaagta ttcatctctg cagaaccccc agacctccct ctgtttctca 180  
 gagtctattc cgacaccctc caacagggag gaaacacaa agaaatccaa cctagagctg 240  
 ctccgcatct cctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt 300  
 gtcttcgcca acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag 360  
 gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact 420  
 gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca 480  
 ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 540  
 ttctgcgca tctgagctg ccgctctgtg gagggcagct gtggcttcgg cggcggcgga 600  
 tcaggcggcg gcggatcagg cggcggcgga tccgaattc 639

<210> 70  
 <211> 206  
 <212> PRT  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 70

Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
 1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
 20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
195 200 205

<210> 71  
<211> 630  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 71  
catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac 60  
cgtctgcacc agctggcctt tgacaccta caggagtttg aagaagccta tatcccaaag 120  
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180  
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac 240  
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc 300  
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360  
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420

ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480  
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540  
atcgtgcagt gccgctctgt ggagggcagc tgtggcttcg gcggcggcgg atcaggcggc 600  
ggcggatcag gcggcggcgg atccgaattc 630

<210> 72  
<211> 206  
<212> PRT  
<213> Artificial  
<220>  
<223> synthetic sequence  
<400> 72

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15  
Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30  
Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45  
Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60  
Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80  
Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95  
Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110  
Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125  
Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140  
Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160  
Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175  
Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
195 200 205

<210> 73  
<211> 1248  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> misc\_feature  
<222> (619)..(1236)  
<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 73  
tgatcattcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac 60  
cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag 120  
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180  
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac 240  
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc 300  
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360  
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420  
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480  
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540  
atcgtgcagt gccgctctgt ggagggcagc tgtggcttcg gcggcggcgg atcaggcggc 600  
ggcggatcag gcggcggcgg atcattccca accattccct tatccaggct ttttgacaac 660  
gctatgctcc gcgcccacg tctgcaccag ctggcctttg acacctacca ggagtttgaa 720  
gaagcctata tcccaaagga acagaagtat tcattcctgc agaacccccca gacctccctc 780  
tgtttctcag agtctattcc gacacctcc aacagggagg aaacacaaca gaaatccaac 840  
ctagagctgc tccgcatctc cctgctgctc atccagtcgt ggctggagcc cgtgcagttc 900  
ctcaggagtg tcttcgcaa cagcctggtg tacggcgcct ctgacagcaa cgtctatgac 960  
ctcctaaagg acctagagga aggcattcaa acgctgatgg ggaggctgga agatggcagc 1020  
ccccggactg ggcagatctt caagcagacc tacagcaagt tcgacacaaa ctacacaaac 1080  
gatgacgcac tactcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag 1140  
gtcgagacat tcttcgcacat cgtgcagtgc cgctctgtgg agggcagctg tggcttcggc 1200



&lt;210&gt; 74

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; synthetic sequence

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (193)..(398)

&lt;223&gt; sequence is repeated N-1 times, where N is a positive whole number

&lt;400&gt; 74

Ser	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu
1				5					10					15	

Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe
		20					25						30		

Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn
	35						40					45			

Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn
	50					55					60				

Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser
65					70					75				80	

Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser
			85					90						95	

Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr
		100						105					110		

Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg
	115					120						125			

Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr
	130					135					140				

Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn
145					150					155				160	

Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr
		165						170						175	

Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe
		180						185					190		

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

195	200	205
Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala 210 215 220		
His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu 225 230 235 240		
Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln 245 250 255		
Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu 260 265 270		
Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu 275 280 285		
Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe 290 295 300		
Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu 305 310 315 320		
Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu 325 330 335		
Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys 340 345 350		
Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly 355 360 365		
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu 370 375 380		
Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly 385 390 395 400		
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly 405 410		

<210> 75  
 <211> 2445  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic sequence

<220>  
 <221> misc\_feature  
 <222> (1237)..(1854)  
 <223> sequence is repeated N-1 times, where N is a positive whole numbe

<400> 75

catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgccc	60
cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag	120
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt	180
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac	240
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcttcaggag tgtcttcgcc	300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag	360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc	420
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag	480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc	540
atcgtgcagt gccgctctgt ggagggcagc tgtggcttgc gcggcgggcg atcaggcggc	600
ggcggatcag gcggcgggcg atcattccca accattccct tatccaggct ttttgacaac	660
gctatgctcc gcgcccacgc tctgcaccag ctggcctttg acacctacca ggagtttgaa	720
gaagcctata tcccaaagga acagaagtat tcattcctgc agaaccacca gacctccctc	780
tgttttctcag agtctattcc gacacctcc aacagggagg aaacacaaca gaaatccaac	840
ctagagctgc tccgcatctc cctgctgctc atccagtcgt ggctggagcc cgtgcagtcc	900
ctcaggagtg tcttcgcca cagcctggtg tacggcgccct ctgacagcaa cgtctatgac	960
ctcctaaagg acctagagga aggcattccaa acgctgatgg ggaggctgga agatggcagc	1020
ccccggactg ggcagatctt caagcagacc tacagcaagt tcgacacaaa ctcacacaac	1080
gatgacgcac tactcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag	1140
gtcgagacat tcttgccat cgtgcagtgc cgctctgtgg agggcagctg tggcttcggc	1200
ggcggcggat caggcggcgg cggatcaggc ggcggcggat cattcccaac cattccctta	1260
tccaggcttt ttgacaacgc tatgctccgc gccatcgctc tgcaccagct ggcctttgac	1320
acctaccagg agtttgaaga agcctatctc ccaaaggaa agaagtattc attcctgcag	1380
aacccccaga cctccctctg tttctcagag tctattccga cacctccaa caggaggaa	1440
acacaacaga aatccaacct agagctgctc cgcattctcc tgetgctcat ccagtcgtgg	1500
ctggagcccc tgcagttcct caggagtgtc ttgcgcaaca gcctggtgta cggcgccctc	1560
gacagcaacg tctatgacct cctaaaggac ctagaggaag gcatccaaac gctgatgggg	1620
aggctggaag atggcagccc ccggactggg cagatcttca agcagacctc cagcaagtcc	1680
gacacaaact cacacaacga tgacgcacta ctcaagaact acgggctgct ctactgcttc	1740

```

aggaaggaca tggacaaggt cgagacattc ctgcgcatcg tgcagtgccg ctctgtggag 1800
ggcagctgtg gcttcggcgg cggcggatca ggcggcggcg gatcaggcgg cggcggatca 1860
ttcccaacca ttcccttata caggtttttt gacaacgcta tgctccgcgc ccatcgtctg 1920
caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag 1980
aagtattcat tctgcagaa cccccagacc tccctctggt tctcagagtc tattccgaca 2040
ccctccaaca gggaggaaac acaacagaaa tccaacctag agctgctccg catctccctg 2100
ctgctcatcc agtcgtgggt ggagcccgtg cagttcctca ggagtgtctt cgccaacagc 2160
ctggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggc 2220
atccaaacgc tgatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag 2280
cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac 2340
gggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcatcgtg 2400
cagtgccgct ctgtggaggg cagctgtggc ttctaggtcg acgcg 2445

```

```

<210> 76
<211> 810
<212> PRT
<213> Artificial

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<220>
<223> synthetic sequence

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<220>
<221> MISC_FEATURE
<222> (412)..(617)
<223> sequence is repeated N-1 times, where N is a positive whole number

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<220>
<221> mat_peptide
<222> (1)..()

```

```

<400> 76

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```

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1           5           10          15

```

```

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
          20           25           30

```

```

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
          35           40           45

```

```

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn

```

50					55					60						
Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	
65					70					75					80	
Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	
			85						90					95		
Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	
			100					105					110			
Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	
			115				120						125			
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	
			130				135						140			
Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	
145					150					155					160	
Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	
				165					170					175		
Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe	
			180					185					190			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Phe	
			195				200						205			
Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu	Arg	Ala	
			210				215					220				
His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe	Glu	Glu	
225					230					235					240	
Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln	
				245					250					255		
Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	
			260					265					270			
Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	
			275				280					285				
Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	
			290				295					300				
Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	
305					310					315					320	
Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	
				325					330					335		
Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	
			340					345					350			
Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	

355	360	365
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu		
370	375	380
Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly		
385	390	395
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Phe Pro Thr		
	405	410
Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg		
	420	425
Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr		
	435	440
Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser		
	450	455
Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr		
	465	470
Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile		
	485	490
Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn		
	500	505
Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys		
	515	520
Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly		
	530	535
Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp		
	545	550
Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu		
	565	570
Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile		
	580	585
Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly Gly Gly		
	595	600
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro		
	610	615
Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His		
	625	630
Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro		
	645	650
Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys		

660	665	670
Phe Ser Glu Ser Ile Pro Thr	Pro Ser Asn Arg Glu Glu Thr Gln Gln	
675	680	685
Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser		
690	695	700
Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu		
705	710	715 720
Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu		
725	730	735
Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro		
740	745	750
Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn		
755	760	765
Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys		
770	775	780
Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln		
785	790	795 800
Cys Arg Ser Val Glu Gly Ser Cys Gly Phe		
805	810	

<210> 77  
 <211> 593  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 77  
 catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac 60  
 cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag 120  
 gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180  
 ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac 240  
 tccctgctgc tcatccagtc gtggttgagg cccgtgcagt tcttcaggag tgtcttcgcc 300  
 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360  
 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420  
 ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480  
 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540  
 atcgtgcagt gccgctctgt ggagggcagc tgtggcttcc atggatcgaa ttc 593

<210> 78  
<211> 192  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 78

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

<210> 79  
<211> 592  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 79



aagctttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc cgcgcccac 60  
gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat atcccaaagg 120  
aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca gagtctattc 180  
cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg ctccgcatct 240  
ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca 300  
acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag gacctagagg 360  
aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccgaggact gggcagatct 420  
tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca ctactcaaga 480  
actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca ttctgcgca 540  
tcgtgcagtg ccgctctgtg gagggcagct gtggcttcca tggatcgaat tc 592

<210> 80  
<211> 191  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 80

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg  
1 5 10 15

Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu  
20 25 30

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro  
35 40 45

Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg  
50 55 60

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu  
65 70 75 80

Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val  
85 90 95

Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp  
100 105 110

Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu  
115 120 125

Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser  
130 135 140

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr  
 145 150 155 160

Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe  
 165 170 175

Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
 180 185 190

<210> 81  
 <211> 587  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 81  
 aagctttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc cgcgcccatc 60  
 gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat atcccaaagg 120  
 aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca gagtctattc 180  
 cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg ctccgcatct 240  
 cctgtctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca 300  
 acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag gacctagagg 360  
 aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact gggcagatct 420  
 tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca ctactcaaga 480  
 actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca ttcttgcgca 540  
 tcgtgcagtg ccgctctgtg gagggcagct gtggcttcta gggatcc 587

<210> 82  
 <211> 191  
 <212> PRT  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 82

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg  
 1 5 10 15

Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu  
 20 25 30

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro

35	40	45
Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg		
50	55	60
Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu		
65	70	75 80
Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val		
	85	90 95
Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp		
	100	105 110
Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu		
	115	120 125
Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser		
	130	135 140
Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr		
	145	150 155 160
Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe		
	165	170 175
Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe		
	180	185 190

<210> 83  
 <211> 1165  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic sequence

<220>  
 <221> misc\_feature  
 <222> (579)..(1151)  
 <223> sequence is repeated N-1 times, where N is a positive whole number

<400> 83  
 aagctttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc cgcgcccac 60  
 gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat atcccaaagg 120  
 aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca gagtctattc 180  
 cgacaccctc caacaggag gaaacacaac agaaatccaa cctagagctg ctccgcatct 240  
 ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca 300  
 acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag gacctagagg 360

aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccggaact gggcagatct 420  
tcaagcagac ctacagcaag ttcgacacaa actcacaçaa cgatgacgca ctactcaaga 480  
actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca ttcctgcgca 540  
tcgtgcagtg ccgctctgtg gagggcagct gtggttctt cccaaccatt cccttatcca 600  
ggctttttga caacgctatg ctccgcgccc atcgtctgca ccagctggcc tttgacacct 660  
accaggagtt tgaagaagcc tatatcccaa aggaacagaa gtattcattc ctgcagaacc 720  
cccagacctc cctctgtttc tcagagtcta ttcgacacc ctccaacagg gaggaaacac 780  
aacagaaatc caacctagag ctgctccgca tctccctgct gctcatccag tcgtggctgg 840  
agcccgtgca gttcctcagg agtgtcttcg ccaacagcct ggtgtacggc gcctctgaca 900  
gcaacgtcta tgacctcta aaggacctag aggaaggcat ccaaacgctg atggggaggc 960  
tggaagatgg cagcccccg actgggcaga tcttcaagca gacctacagc aagttcgaca 1020  
caaactcaca caacgatgac gcactactca agaactacgg gctgctctac tgcttcagga 1080  
aggacatgga caaggctgag acattcctgc gcacgtgca gtgccgctct gtggagggca 1140  
gctgtggctt ccatggatcg aattc 1165

<210> 84

<211> 191

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC\_FEATURE

<222> (1)..(191)

<223> sequence is repeated N times, where N is a positive whole number

<400> 84

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg  
1 5 10 15

Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu  
20 25 30

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro  
35 40 45

Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg  
50 55 60

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu  
65 70 75 80

Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val  
85 90 95

Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp  
100 105 110

Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu  
115 120 125

Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser  
130 135 140

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr  
145 150 155 160

Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe  
165 170 175

Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

<210> 85  
<211> 2307  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> misc\_feature  
<222> (1153)..(1725)  
<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 85  
catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac 60  
cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag 120  
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180  
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac 240  
tcctgctgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc 300  
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360  
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420  
ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag 480

aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgagc	540
atcgtgcagt gccgctctgt ggagggcagc tgtggcttct tcccaaccat tcccttatcc	600
aggctttttg acaacgctat gtccegcgcc catcgtctgc accagctggc ctttgacacc	660
taccaggagt ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac	720
ccccagacct ccctctgttt ctcagagtct attccgacac cctccaacag ggaggaaaca	780
caacagaaat ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg	840
gagcccgctg agttcctcag gagtgtcttc gccaacagcc tgggtgtacgg cgcctctgac	900
agcaacgtct atgacctcct aaaggacctt gaggaaggca tccaaacgct gatggggagg	960
ctggaagatg gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac	1020
acaaactcac acaacgatga cgcactactc aagaactacg ggctgctcta ctgcttcagg	1080
aaggacatgg acaaggctga gacattcctg cgcacgtgctc agtgccgctc tgtggagggc	1140
agctgtggct tcttcccaac cattccctta tccaggcttt ttgacaacgc tatgctccgc	1200
gcccatcgct tgcaccagct ggcttttgac acctaccagg agtttgaaga agcctatatt	1260
ccaaaggaaac agaagtattc attcctgcag aacccccaga cctccctctg tttctcagag	1320
tctattccga caccctcaa cagggaggaa acacaacaga aatccaacct agagctgctc	1380
cgcactctcc tgctgctcat ccagtcgtgg ctggagcccg tgcagttcct caggagtgtc	1440
ttcgccaaca gcctgggtga cggcgctct gacagcaacg tctatgacct cctaaaggac	1500
ctagaggaag gcatccaaac gctgatgggg aggctggaag atggcagccc ccggactggg	1560
cagatcttca agcagacctt cagcaagttc gacacaaact cacacaacga tgacgcacta	1620
ctcaagaact acgggctgct ctactgcttc aggaaggaca tggacaaggc cgagacattc	1680
ctgcgcacgt tgcagtgcg ctctgtggag ggcagctgtg gcttcttccc aaccattccc	1740
ttatccaggc tttttgacaa cgctatgctc cgcgcccatc gtctgcacca gctggccttt	1800
gacacctacc aggagtttga agaagcctat atcccaaagg aacagaagta ttcattcctg	1860
cagaaccccc agacctcct ctgtttctca gagtctattc cgacaccctc caacagggag	1920
gaaacacaac agaaatcaa cctagagctg ctccgcatct cctgctgct catccagtcg	1980
tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca acagcctggc gtacggcgcc	2040
tctgacagca acgtctatga cctcctaaag gacctagagg aaggcatcca aacgctgatg	2100
gggaggctgg aagatggcag cccccggact gggcagatct tcaagcagac ctacagcaag	2160
ttcgacacaa actcacacaa cgatgacgca ctactcaaga actacgggct gctctactgc	2220

ttcaggaagg acatggacaa ggtcgagaca ttcctgcgca tcgtgcagtg ccgctctgtg 2280  
gagggcagct gtggcttcta gggatcc 2307

<210> 86  
<211> 192  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> MISC\_FEATURE  
<222> (2)..(192)  
<223> sequence is repeated N+2 times, where N is a positive whole numbe

<220>  
<221> mat\_peptide  
<222> (1)..()

<400> 86

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190